

Appendix I: Alignment of instant SEQ ID NO: 2 and GenBank Accession No. XM_051900

BLASTN 2.2.22+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: SK5US79Y114

Query= SID_2
Length=3356

Sequences producing significant alignments:	Score (Bits)	E Value
ref XM_051900.1 Homo sapiens prostaglandin-endoperoxide synt...	6198	0.0

ALIGNMENTS

>ref|XM_051900.1| Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA
Length=3356

Score = 6198 bits (3356), Expect = 0.0
Identities = 3356/3356 (100%), Gaps = 0/3356 (0%)
Strand=Plus/Plus

Query	1	GTCCAGGAACCTCCTCAGCAGCGCCTCCTTCAGCTCCACAGCCAGACGCCCTCAGACAGCA	60
Sbjct	1	GTCCAGGAACCTCCTCAGCAGCGCCTCCTTCAGCTCCACAGCCAGACGCCCTCAGACAGCA	60
Query	61	AAGCCTACCCCGCGCGCGCCCTGCCCGCCGCTGCGATGCTCGCCCGCGCCCTGCTGCT	120
Sbjct	61	AAGCCTACCCCGCGCGCGCCCTGCCCGCCGCTGCGATGCTCGCCCGCGCCCTGCTGCT	120
Query	121	GTGCGCGGTCCTGGCGCTCAGCCATACAGCAAATCCTTGCTGTTCCACCCATGTCAAAA	180
Sbjct	121	GTGCGCGGTCCTGGCGCTCAGCCATACAGCAAATCCTTGCTGTTCCACCCATGTCAAAA	180
Query	181	CCGAGGTGTATGTATGAGTGTGGGATTTGACCAGTATAAGTGCGATTGTACCCGGACAGG	240
Sbjct	181	CCGAGGTGTATGTATGAGTGTGGGATTTGACCAGTATAAGTGCGATTGTACCCGGACAGG	240
Query	241	ATTCTATGGAGAAAACCTGCTCAACACCGGAATTTTGGACAAGAATAAAATTATTTCTGAA	300
Sbjct	241	ATTCTATGGAGAAAACCTGCTCAACACCGGAATTTTGGACAAGAATAAAATTATTTCTGAA	300
Query	301	ACCCACTCCAAACACAGTGCACTACATACTTACCCACTTCAAGGGATTTTGGAAACGTTGT	360
Sbjct	301	ACCCACTCCAAACACAGTGCACTACATACTTACCCACTTCAAGGGATTTTGGAAACGTTGT	360
Query	361	GAATAACATTCCCTTCCTTCGAAATGCAATTATGAGTTATGTGTTGACATCCAGATCACA	420
Sbjct	361	GAATAACATTCCCTTCCTTCGAAATGCAATTATGAGTTATGTGTTGACATCCAGATCACA	420
Query	421	TTTGATTGACAGTCCACCAACTTACAATGCTGACTATGGCTACAAAAGCTGGGAAGCCTT	480
Sbjct	421	TTTGATTGACAGTCCACCAACTTACAATGCTGACTATGGCTACAAAAGCTGGGAAGCCTT	480
Query	481	CTCTAACCTCTCCTATTATACTAGAGCCCTTCCTCCTGTGCCTGATGATTGCCCGACTCC	540

Sbjct	481	 CTCTAACCTCTCCTATTATACTAGAGCCCTTCCTCCTGTGCCTGATGATTGCCCCGACTCC	540
Query	541	CTTGGGTGTCAAAGGTAAAAAGCAGCTTCCTGATTCAAATGAGATTGTGGAAAAATTGCT	600
Sbjct	541	 CTTGGGTGTCAAAGGTAAAAAGCAGCTTCCTGATTCAAATGAGATTGTGGAAAAATTGCT	600
Query	601	TCTAAGAAGAAAGTTTCATCCCTGATCCCCAGGGCTCAAACATGATGTTTGCATTCTTTGC	660
Sbjct	601	 TCTAAGAAGAAAGTTTCATCCCTGATCCCCAGGGCTCAAACATGATGTTTGCATTCTTTGC	660
Query	661	CCAGCACTTCACGCATCAGTTTTTCAAGACAGATCATAAGCGAGGGCCAGCTTTCACCAA	720
Sbjct	661	 CCAGCACTTCACGCATCAGTTTTTCAAGACAGATCATAAGCGAGGGCCAGCTTTCACCAA	720
Query	721	CGGGCTGGGCCATGGGGTGGACTTAAATCATATTTACGGTGAAACTCTGGCTAGACAGCG	780
Sbjct	721	 CGGGCTGGGCCATGGGGTGGACTTAAATCATATTTACGGTGAAACTCTGGCTAGACAGCG	780
Query	781	TAAACTGCGCCTTTTCAAGGATGGAAAAATGAAATATCAGATAATTGATGGAGAGATGTA	840
Sbjct	781	 TAAACTGCGCCTTTTCAAGGATGGAAAAATGAAATATCAGATAATTGATGGAGAGATGTA	840
Query	841	TCCTCCACAGTCAAAGATACTCAGGCAGAGATGATCTACCCTCCTCAAGTCCCTGAGCA	900
Sbjct	841	 TCCTCCACAGTCAAAGATACTCAGGCAGAGATGATCTACCCTCCTCAAGTCCCTGAGCA	900
Query	901	TCTACGGTTTGCTGTGGGGCAGGAGGTCTTTGGTCTGGTGCCTGGTCTGATGATGTATGC	960
Sbjct	901	 TCTACGGTTTGCTGTGGGGCAGGAGGTCTTTGGTCTGGTGCCTGGTCTGATGATGTATGC	960
Query	961	CACAATCTGGCTGCGGGAACACAACAGAGTATGCGATGTGCTTAAACAGGAGCATCCTGA	1020
Sbjct	961	 CACAATCTGGCTGCGGGAACACAACAGAGTATGCGATGTGCTTAAACAGGAGCATCCTGA	1020
Query	1021	ATGGGGTGATGAGCAGTTGTTCCAGACAAGCAGGCTAATACTGATAGGAGAGACTATTAA	1080
Sbjct	1021	 ATGGGGTGATGAGCAGTTGTTCCAGACAAGCAGGCTAATACTGATAGGAGAGACTATTAA	1080
Query	1081	GATTGTGATTGAAGATTATGTGCAACACTTGAGTGGCTATCACTTCAAACGAAATTTGA	1140
Sbjct	1081	 GATTGTGATTGAAGATTATGTGCAACACTTGAGTGGCTATCACTTCAAACGAAATTTGA	1140
Query	1141	CCCAGAACTACTTTTCAACAAACAATTCCAGTACCAAATCGTATTGCTGCTGAATTTAA	1200
Sbjct	1141	 CCCAGAACTACTTTTCAACAAACAATTCCAGTACCAAATCGTATTGCTGCTGAATTTAA	1200
Query	1201	CACCCTCTATCACTGGCATCCCCTTCTGCCTGACACCTTTCAAATTCATGACCAGAAATA	1260
Sbjct	1201	 CACCCTCTATCACTGGCATCCCCTTCTGCCTGACACCTTTCAAATTCATGACCAGAAATA	1260
Query	1261	CAACTATCAACAGTTTATCTACAACAACCTCTATATTGCTGGAACATGGAATTACCCAGTT	1320
Sbjct	1261	 CAACTATCAACAGTTTATCTACAACAACCTCTATATTGCTGGAACATGGAATTACCCAGTT	1320
Query	1321	TGTTGAATCATTACCAGGCAAATTGCTGGCAGGGTTGCTGGTGGTAGGAATGTTCCACC	1380
Sbjct	1321	 TGTTGAATCATTACCAGGCAAATTGCTGGCAGGGTTGCTGGTGGTAGGAATGTTCCACC	1380
Query	1381	CGCAGTACAGAAAGTATCACAGGCTTCCATTGACCAGAGCAGGCAGATGAAATACCAGTC	1440

Sbjct	1381	 CGCAGTACAGAAAGTATCACAGGCTTCCATTGACCAGAGCAGGCAGATGAAATACCAGTC	1440
Query	1441	TTTTAATGAGTACCGCAAACGCTTTATGCTGAAGCCCTATGAATCATTTGAAGAACTTAC	1500
Sbjct	1441	 TTTTAATGAGTACCGCAAACGCTTTATGCTGAAGCCCTATGAATCATTTGAAGAACTTAC	1500
Query	1501	AGGAGAAAAGGAAATGTCTGCAGAGTTGGAAGCACTCTATGGTGACATCGATGCTGTGGA	1560
Sbjct	1501	 AGGAGAAAAGGAAATGTCTGCAGAGTTGGAAGCACTCTATGGTGACATCGATGCTGTGGA	1560
Query	1561	GCTGTATCCTGCCCTTCTGGTAGAAAAGCCTCGGCCAGATGCCATCTTTGGTGAAACCAT	1620
Sbjct	1561	 GCTGTATCCTGCCCTTCTGGTAGAAAAGCCTCGGCCAGATGCCATCTTTGGTGAAACCAT	1620
Query	1621	GGTAGAAGTTGGAGCACCATTCTCCTTGAAAGGACTTATGGGTAATGTTATATGTTCTCC	1680
Sbjct	1621	 GGTAGAAGTTGGAGCACCATTCTCCTTGAAAGGACTTATGGGTAATGTTATATGTTCTCC	1680
Query	1681	TGCCTACTGGAAGCCAAGCACTTTTGGTGGAGAAGTGGGTTTTCAAATCATCAACACTGC	1740
Sbjct	1681	 TGCCTACTGGAAGCCAAGCACTTTTGGTGGAGAAGTGGGTTTTCAAATCATCAACACTGC	1740
Query	1741	CTCAATTCAGTCTCTCATCTGCAATAACGTGAAGGGCTGTCCCTTTACTTCATTTCAGTGT	1800
Sbjct	1741	 CTCAATTCAGTCTCTCATCTGCAATAACGTGAAGGGCTGTCCCTTTACTTCATTTCAGTGT	1800
Query	1801	TCCAGATCCAGAGCTCATTAAACAGTCACCATCAATGCAAGTTCTTCCCGCTCCGGACT	1860
Sbjct	1801	 TCCAGATCCAGAGCTCATTAAACAGTCACCATCAATGCAAGTTCTTCCCGCTCCGGACT	1860
Query	1861	AGATGATATCAATCCCACAGTACTACTAAAAGAACGTTGACTGAACTGTAGAAGTCTAA	1920
Sbjct	1861	 AGATGATATCAATCCCACAGTACTACTAAAAGAACGTTGACTGAACTGTAGAAGTCTAA	1920
Query	1921	TGATCATATTTATTTATTTATATGAACCATGTCTATTAATTTAATTATTTAATAATATTT	1980
Sbjct	1921	 TGATCATATTTATTTATTTATATGAACCATGTCTATTAATTTAATTATTTAATAATATTT	1980
Query	1981	ATATTAAACTCCTTATGTTACTTAAACATCTTCTGTAACAGAAGTCAGTACTCCTGTTGCG	2040
Sbjct	1981	 ATATTAAACTCCTTATGTTACTTAAACATCTTCTGTAACAGAAGTCAGTACTCCTGTTGCG	2040
Query	2041	GAGAAAGGAGTCATACTTGTGAAGACTTTTATGTCACTACTCTAAAGATTTTGCTGTTGC	2100
Sbjct	2041	 GAGAAAGGAGTCATACTTGTGAAGACTTTTATGTCACTACTCTAAAGATTTTGCTGTTGC	2100
Query	2101	TGTTAAGTTTGGAACAGTTTTTATTCTGTTTTATAAACAGAGAGAAATGAGTTTTGA	2160
Sbjct	2101	 TGTTAAGTTTGGAACAGTTTTTATTCTGTTTTATAAACAGAGAGAAATGAGTTTTGA	2160
Query	2161	CGTCTTTTTACTTGAATTTCAACTTATATTATAAGAACGAAAGTAAAGATGTTTGAATAC	2220
Sbjct	2161	 CGTCTTTTTACTTGAATTTCAACTTATATTATAAGAACGAAAGTAAAGATGTTTGAATAC	2220
Query	2221	TTAAACACTGTCACAAGATGGCAAAATGCTGAAAGTTTTTACACTGTCGATGTTTCCAAT	2280
Sbjct	2221	 TTAAACACTGTCACAAGATGGCAAAATGCTGAAAGTTTTTACACTGTCGATGTTTCCAAT	2280
Query	2281	GCATCTTCATGATGCATTAGAAGTAACTAATGTTTGAAATTTTAAAGTACTTTTGGTTA	2340

Sbjct	2281	 GCATCTTCCATGATGCATTAGAAAGTAACTAATGTTTGAAATTTTAAAGTACTTTTGGTTA	2340
Query	2341	TTTTTCTGTCATCAAACAAAAACAGGTATCAGTGCATTATTAAATGAATATTTAAATTAG	2400
Sbjct	2341	 TTTTTCTGTCATCAAACAAAAACAGGTATCAGTGCATTATTAAATGAATATTTAAATTAG	2400
Query	2401	ACATTACCAGTAATTTTCATGTCTACTTTTTTAAATCAGCAATGAAACAATAATTTGAAAT	2460
Sbjct	2401	 ACATTACCAGTAATTTTCATGTCTACTTTTTTAAATCAGCAATGAAACAATAATTTGAAAT	2460
Query	2461	TTCTAAATTCATAGGGTAGAATCACCTGTAAAAGCTTGTTTGATTTCTTAAAGTTATTAA	2520
Sbjct	2461	 TTCTAAATTCATAGGGTAGAATCACCTGTAAAAGCTTGTTTGATTTCTTAAAGTTATTAA	2520
Query	2521	ACTTGTACATATACCAAAAAGAAGCTGTCTTGGATTTAAATCTGTAAAATCAGTAGAAAT	2580
Sbjct	2521	 ACTTGTACATATACCAAAAAGAAGCTGTCTTGGATTTAAATCTGTAAAATCAGTAGAAAT	2580
Query	2581	TTTACTACAATTGCTTGTTAAAATATTTTATAAGTGATGTTTCCTTTTTCACCAAGAGTAT	2640
Sbjct	2581	 TTTACTACAATTGCTTGTTAAAATATTTTATAAGTGATGTTTCCTTTTTCACCAAGAGTAT	2640
Query	2641	AAACCTTTTTTAGTGTGACTGTTAAAACCTTCCTTTTAAATCAAATGCCAAATTTATTAAG	2700
Sbjct	2641	 AAACCTTTTTTAGTGTGACTGTTAAAACCTTCCTTTTAAATCAAATGCCAAATTTATTAAG	2700
Query	2701	GTGGTGGAGCCACTGCAGTGTTATCTTAAAATAAGAATATTTTGTTGAGATATTCCAGAA	2760
Sbjct	2701	 GTGGTGGAGCCACTGCAGTGTTATCTTAAAATAAGAATATTTTGTTGAGATATTCCAGAA	2760
Query	2761	TTTGTTTATATGGCTGGTAACATGTAAAATCTATATCAGCAAAAGGGTCTACCTTTAAAA	2820
Sbjct	2761	 TTTGTTTATATGGCTGGTAACATGTAAAATCTATATCAGCAAAAGGGTCTACCTTTAAAA	2820
Query	2821	TAAGCAATAACAAAGAAGAAAACCAAATTATTGTTCAAATTTAGGTTTAACTTTTGAAG	2880
Sbjct	2821	 TAAGCAATAACAAAGAAGAAAACCAAATTATTGTTCAAATTTAGGTTTAACTTTTGAAG	2880
Query	2881	CAAACCTTTTTTTTATCCTTGTGCACTGCAGGCCTGGTACTCAGATTTTGCTATGAGGTTA	2940
Sbjct	2881	 CAAACCTTTTTTTTATCCTTGTGCACTGCAGGCCTGGTACTCAGATTTTGCTATGAGGTTA	2940
Query	2941	ATGAAGTACCAAGCTGTGCTTGAATAATGATATGTTTTCTCAGATTTTCTGTTGTACAGT	3000
Sbjct	2941	 ATGAAGTACCAAGCTGTGCTTGAATAATGATATGTTTTCTCAGATTTTCTGTTGTACAGT	3000
Query	3001	TTAATTTAGCAGTCCATATCACATTGCAAAAGTAGCAATGACCTCATAAAATACCTCTTC	3060
Sbjct	3001	 TTAATTTAGCAGTCCATATCACATTGCAAAAGTAGCAATGACCTCATAAAATACCTCTTC	3060
Query	3061	AAAATGCTTAAATTCATTTACACATTAATTTTATCTCAGTCTTGAAGCCAATTCAGTAG	3120
Sbjct	3061	 AAAATGCTTAAATTCATTTACACATTAATTTTATCTCAGTCTTGAAGCCAATTCAGTAG	3120
Query	3121	GTGCATTGGAATCAAGCCTGGCTACCTGCATGCTGTTTCCTTTTCTTTCTTTTAGCC	3180
Sbjct	3121	 GTGCATTGGAATCAAGCCTGGCTACCTGCATGCTGTTTCCTTTTCTTTCTTTTAGCC	3180
Query	3181	ATTTTGCTAAGAGACACAGTCTTCTCATCACTTCGTTTCTCCTATTTTGTTTTACTAGTT	3240

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Sbjct  3181  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ATTTTGCTAAGAGACACAGTCTTCTCATCACTTCGTTTCTCCTATTTTGTTTTACTAGTT  3240
Query   3241  TTAAGATCAGAGTTCACCTTTCTTTGGACTCTGCCTATATTTTCTTACCTGAACTTTTGCA  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3241  TTAAGATCAGAGTTCACCTTTCTTTGGACTCTGCCTATATTTTCTTACCTGAACTTTTGCA  3300
Query   3301  AGTTTTCAGGTAAACCTCAGCTCAGGACTGCTATTTAGCTCCTCTTAAGAAGATTA  3356
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3301  AGTTTTCAGGTAAACCTCAGCTCAGGACTGCTATTTAGCTCCTCTTAAGAAGATTA  3356
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